

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Somerville, Chris  
Broun, Pierre  
van de Loo, Frank  
Boddupalli, Sekhar S.
- (ii) TITLE OF INVENTION: Production of Hydroxylated Fatty Acids in Genetically Modified Plants
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: PILLSBURY MADISON & SUTRO  
(B) STREET: 1100 NEW YORK AVENUE, N.W.  
(C) CITY: WASHINGTON  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20005-3918
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 MB storage  
(B) COMPUTER: IBM compatible  
(C) OPERATING SYSTEM: DOS 5.0  
(D) SOFTWARE: Word Perfect 5.1
- (vi) CURRENT APPLICATION DATA;  
(A) APPLICATION NUMBER: not yet assigned  
(B) FILING DATE: February 6, 1997  
(C) CLASSIFICATION:

## (2) INFORMATION FOR SEQ ID NO:1

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 543 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATTGGCACC GCGGGCACCA TTCCAACAAT GGATCCCTAG 40  
AAAAAGATGA AGTCTTTGTC CCACCTAAGA AAGCTGCAGT 80  
CANATGGTAT GTCAAATACC TCAACAACCC TCTTGGACGC 120  
ATTCTGGTGT TAACAGTTCA GTTTATCCTC GGGTGGCCTT 160

6543210

Sub  
a1

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 544 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	40
AAAGAGATGA	AGTATTGTGTC	CCAAAGCAGA	AATCCGCAAT	80
CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTTCGC	120
ATCATGATGT	TAAGTGTCCA	GTTCGTCTCT	GGATGGCCCT	160
TGTACTTAGC	CTTCAACGTT	TCTGGCAGAC	CCTACAATGG	200
TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAAC	240
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	280
TTCTAGCCGT	CTGTTATGGT	CTTTACCGTT	ACGCTGTTGC	320
ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG	360
CTTCTGATAG	TTAACTTTTT	CCTCGTCTTG	ATCACTTACT	400

ATGAAGCTTT	ATAAGAAGTT	AGTTTTCTCT	GGTGACAGAG	40
AAATTNTGTC	AATTGGTAGT	GACAGTTGAA	GCAACAGGAA	80
CAACAAGGAT	GGTTGGTGNT	GATGCTGATG	TGGTGATGTG	120
TTATTCATCA	AATACTAAAT	ACTACATTAC	TTGTTGCTGC	160
CTACTTCTCC	TATTTCTCC	GCCACCCATT	TTGGACCCAC	200
GANCCTTCCA	TTTAAACCCT	CTCTCGTGCT	ATTCACCAGA	240
AGAGAAGCCA	AGAGAGAGAG	AGAGAGAATG	TTCTGAGGAT	280
CATTGTCTTC	TTCATCGTTA	TTAACGTAAG	TTTTTTTTGA	320
CCACTCATAT	CTAAAATCTA	GTACATGCAA	TAGATTAATG	360
ACTGTTCTTT	CTTTTGATAT	TTTCAGCTTC	TTGAATTCAA	400
GATGGGTGCT	GGTGGAAGAA	TAATGGTTAC	CCCCTCTTCC	440
AAGAAATCAG	AAACTGAAGC	CCTAAAACGT	GGACCATGTG	480
AGAAACCACC	ATTCACTGTT	AAAGATCTGA	AGAAAGCAAT	520
CCCACAGCAT	TGTTTCAAGC	GCTCTATCCC	TCGTTCTTTC	560
TCCTACCTTC	TCACAGATAT	CACTTTAGTT	TCTTGCTTCT	600
ACTACGTTGC	CACAAATTAC	TTCTCTCTTC	TTCTCAGCC	640

Sub  
a  
ant

TCTCTCTACT TACCTAGCTT GGCCTCTCTA TTGGGTATGT 680  
CAAGGCTGTG TCTTAACCGG TATCTGGGTC ATTGGCCATG 720  
AATGTGGTCA CCATGCATTG AGTGACTATC AATGGGTAGA 760  
TGACACTGTT GGTTTTATCT TCCATTCCTT CCTTCTCGTC 800  
CCTTACTTCT CCTGGAAATA CAGTCATCGT CGTCACCATT 840  
CCAACAATGG ATCTCTCGAG AAAGATGAAG TCTTTGTCCC 880  
ACCGAAGAAA GCTGCAGTCA AATGGTATGT TAAATACCTC 920  
AACAACCCTC TTGGACGCAT TCTGGTGTTA ACAGTTCAGT 960  
TTATCCTCGG GTGGCCTTTG TATCTAGCCT TTAATGTATC 1000  
AGGTAGACCT TATGATGGTT TCGCTTCACA TTTCTTCCCT 1040  
CATGCACCTA TCTTTAAAGA CCGAGAACGC CTCCAGATAT 1080  
ACATCTCAGA TGCTGGTATT CTAGCTGTCT GTTATGGTCT 1120  
TTACCGTTAC GCTGCTTCAC AAGGATTGAC TGCTATGATC 1160  
TGCCTCTATG GAGTACCGCT TTTGATAGTG AACTTTTTCC 1200  
TTGTCTTGGT AACTTTCTTG CAGCACACTC ATCCTTCGTT 1240  
ACCTCATTAT GATTCAACCG AGTGGGAATG GATTAGAGGA 1280  
GCTTTGGTTA CGGTAGACAG AGACTATGGA ATATTGAACA 1320  
AGGTGTTCCA TAACATAACA GACACACATG TGGCTCATCA 1360  
TCTCTTTGCA ACTATACCGC ATTATAACGC AATGGAAGCT 1400  
ACAGAGGCGA TAAAGCCAAT ACTTGGTGAT TACTACCACT 1440  
TCGATGGAAC ACCGTGGTAT GTGGCCATGT ATAGGGAAGC 1480  
AAAGGAGTGT CTCTATGTAG AACCGGATAC GGAACGTGGG 1520  
AAGAAAGGTG TCTACTATTA CAACAATAAG TTATGAGGCT 1560  
GATAGGGCGA GAGAAGTGCA ATTATCAATC TTCATTTCCT 1600  
TGTTTTAGGT GTCTTGTTTA AGAAGCTATG CTTTGTTTCA 1640  
ATAATCTCAG AGTCCATNTA GTTGTGTTCT GGTGCATTTT 1680

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cont.

GCCTAGTTAT GTGGTGTCTGG AAGTTAGTGT TCAAACCTGCT 1720  
 TCCTGCTGTG CTGCCCAGTG AAGAACAAGT TTACGTGTTT 1760  
 AAAATACTCG GAACGAATTG ACCACAAAT ATCCAAAACC 1800  
 GGCTATCCGA ATTCCATATC CGAAAACCGG ATATCCAAAT 1840  
 TTCCAGAGTA CTTAG 1855

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Gly Gly Arg Ile Met Val Thr  
                                   5                                  10  
 Pro Ser Ser Lys Lys Ser Glu Thr Glu Ala  
                                   15                                  20  
 Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro  
                                   25                                  30  
 Phe Thr Val Lys Asp Leu Lys Lys Ala Ile  
                                   35                                  40  
 Pro Gln His Cys Phe Lys Arg Ser Ile Pro  
                                   45                                  50  
 Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile  
                                   55                                  60  
 Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala  
                                   65                                  70  
 Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
                                   75                                  80  
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr  
                                   85                                  90  
 Trp Val Cys Gln Gly Cys Val Leu Thr Gly  
                                   95                                  100

*Sub  
a1  
cont.*

Ile Trp Val Ile Gly His Glu Cys Gly His  
 105 110  
 His Ala Phe Ser Asp Tyr Gln Trp Val Asp  
 115 120  
 Asp Thr Val Gly Phe Ile Phe His Ser Phe  
 125 130  
 Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
 135 140  
 Ser His Arg Arg His His Ser Asn Asn Gly  
 145 150  
 Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
 155 160  
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val  
 165 170  
 Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile  
 175 180  
 Leu Val Leu Thr Val Gln Phe Ile Leu Gly  
 185 190  
 Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser  
 195 200  
 Gly Arg Pro Tyr Asp Gly Phe Ala Ser His  
 205 210  
 Phe Phe Pro His Ala Pro Ile Phe Lys Asp  
 215 220  
 Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp  
 225 230  
 Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 235 240  
 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr  
 245 250  
 Ala Met Ile Cys Val Tyr Gly Val Pro Leu  
 255 260  
 Leu Ile Val Asn Phe Phe Leu Val Leu Val  
 265 270

Sub  
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 cont

Thr Phe Leu Gln His Thr His Pro Ser Leu  
 275 280  
 Pro His Tyr Asp Ser Thr Glu Trp Glu Trp  
 285 290  
 Ile Arg Gly Ala Leu Val Thr Val Asp Arg  
 295 300  
 Asp Tyr Gly Ile Leu Asn Lys Val Phe His  
 305 310  
 Asn Ile Thr Asp Thr His Val Ala His His  
 315 320  
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala  
 325 330  
 Met Glu Ala Thr Glu Ala Ile Lys Pro Ile  
 335 340  
 Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr  
 345 350  
 Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala  
 355 360  
 Lys Glu Cys Leu Tyr Val Glu Pro Asp Thr  
 365 370  
 Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr  
 375 380  
 Asn Asn Lys Leu

## (2) INFORMATION FOR SEQ ID NO:5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Gly Gly Gly Arg Met Ser Thr Val  
 5 10  
 Ile Thr Ser Asn Asn Ser Glu Lys Lys Gly  
 15 20

Sub  
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 Cont-

Gly Ser Ser His Leu Lys Arg Ala Pro His  
 25 30  
 Thr Lys Pro Pro Phe Thr Leu Gly Asp Leu  
 35 40  
 Lys Arg Ala Ile Pro Pro His Cys Phe Glu  
 45 50  
 Arg Ser Phe Val Arg Ser Phe Ser Tyr Val  
 55 60  
 Ala Tyr Asp Val Cys Leu Ser Phe Leu Phe  
 65 70  
 Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 75 80  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp  
 85 90  
 Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile  
 95 100  
 Leu Thr Gly Leu Trp Val Ile Gly His Glu  
 105 110  
 Cys Gly His His Ala Phe Ser Glu Tyr Gln  
 115 120  
 Leu Ala Asp Asp Ile Val Gly Leu Ile Val  
 125 130  
 His Ser Ala Leu Leu Val Pro Tyr Phe Ser  
 135 140  
 Trp Lys Tyr Ser His Arg Arg His His Ser  
 145 150  
 Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 155 160  
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser  
 165 170  
 Trp Tyr Ser Lys Tyr Ser Asn Asn Pro Pro  
 175 180  
 Gly Arg Val Leu Thr Leu Ala Ala Thr Leu  
 185 190

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Leu	Leu	Gly	Trp	Pro	Leu	Tyr	Leu	Ala	Phe
				195					200
Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Arg	Phe
				205					210
Ala	Cys	His	Tyr	Asp	Pro	Tyr	Gly	Pro	Ile
				215					220
Phe	Ser	Glu	Arg	Glu	Arg	Leu	Gln	Ile	Tyr
				225					230
Ile	Ala	Asp	Leu	Gly	Ile	Phe	Ala	Thr	Thr
				235					240
Phe	Val	Leu	Tyr	Gln	Ala	Thr	Met	Ala	Lys
				245					250
Gly	Leu	Ala	Trp	Val	Met	Arg	Ile	Tyr	Gly
				255					260
Val	Pro	Leu	Leu	Ile	Val	Asn	Cys	Phe	Leu
				265					270
Val	Met	Ile	Thr	Tyr	Leu	Gln	His	Thr	His
				275					280
Pro	Ala	Ile	Pro	Arg	Tyr	Gly	Ser	Ser	Glu
				285					290
Trp	Asp	Trp	Leu	Arg	Gly	Ala	Met	Val	Thr
				295					300
Val	Asp	Arg	Asp	Tyr	Gly	Val	Leu	Asn	Lys
				305					310
Val	Phe	His	Asn	Ile	Ala	Asp	Thr	His	Val
				315					320
Ala	His	His	Leu	Phe	Ala	Thr	Val	Pro	His
				325					330
Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile
				335					340
Lys	Pro	Ile	Met	Gly	Glu	Tyr	Tyr	Arg	Tyr
				345					350
Asp	Gly	Thr	Pro	Phe	Tyr	Lys	Ala	Leu	Trp
				355					360

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Arg Glu Ala Lys Glu Cys Leu Phe Val Glu  
365 370

Pro Asp Glu Gly Ala Pro Thr Gln Gly Val  
375 380

Phe Trp Tyr Arg Asn Lys Tyr  
385

(2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Gly Gly Arg Met Pro Val Pro  
5 10

Thr Ser Ser Lys Lys Ser Glu Thr Asp Thr  
15 20

Thr Lys Arg Val Pro Cys Glu Lys Pro Pro  
25 30

Phe Ser Val Gly Asp Leu Lys Lys Ala Ile  
35 40

Pro Pro His Cys Phe Lys Arg Ser Ile Pro  
45 50

Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile  
55 60

Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala  
65 70

Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
75 80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp  
85 90

Ala Cys Gln Gly Cys Val Leu Thr Gly Ile  
95 100

Trp Val Ile Ala His Glu Cys Gly His His  
105 110

Sequence of amino acids

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Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp  
 115 120  
 Thr Val Gly Leu Ile Phe His Ser Phe Leu  
 125 130  
 Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 135 140  
 His Arg Arg His His Ser Asn Thr Gly Ser  
 145 150  
 Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 155 160  
 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys  
 165 170  
 Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met  
 175 180  
 Met Leu Thr Val Gln Phe Val Leu Gly Trp  
 185 190  
 Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly  
 195 200  
 Arg Pro Tyr Asp Gly Phe Ala Cys His Phe  
 205 210  
 Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg  
 215 220  
 Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala  
 225 230  
 Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr  
 235 240  
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser  
 245 250  
 Met Ile Cys Leu Tyr Gly Val Pro Leu Leu  
 255 260  
 Ile Val Asn Ala Phe Leu Val Leu Ile Thr  
 265 270  
 Tyr Leu Gln His Thr His Pro Ser Leu Pro  
 275 280

Sub  
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His Tyr Asp Ser Ser Glu Trp Asp Trp Leu  
 285 290  
 Arg Gly Ala Leu Ala Thr Val Asp Arg Asp  
 295 300  
 Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
 305 310  
 Ile Thr Asp Thr His Val Ala His His Leu  
 315 320  
 Phe Ser Thr Met Pro His Tyr Asn Ala Met  
 325 330  
 Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu  
 335 340  
 Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro  
 345 350  
 Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys  
 355 360  
 Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu  
 365 370  
 Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn  
 375 380  
 Asn Lys Leu

## (2) INFORMATION FOR SEQ ID NO:7

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Ala Gly Gly Arg Met Gln Val Ser  
 5 10  
 Pro Pro Ser Lys Lys Ser Glu Thr Asp Asn  
 15 20  
 Ile Lys Arg Val Pro Cys Glu Thr Pro Pro  
 25 30

Subl  
 at  
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Phe Thr Val Gly Glu Leu Lys Lys Ala Ile  
 35 40  
 Pro Pro His Cys Phe Lys Arg Ser Ile Pro  
 45 50  
 Arg Ser Phe Ser His Leu Ile Trp Asp Ile  
 55 60  
 Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala  
 65 70  
 Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro  
 75 80  
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp  
 85 90  
 Ala Cys Gln Gly Cys Val Leu Thr Gly Val  
 95 100  
 Trp Val Ile Ala His Glu Cys Gly His Ala  
 105 110  
 Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp  
 115 120  
 Thr Val Gly Leu Ile Phe His Ser Phe Leu  
 125 130  
 Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 135 140  
 His Arg Arg His His Ser Asn Thr Gly Ser  
 145 150  
 Leu Glu Arg Asp Glu Val Phe Val Pro Arg  
 155 160  
 Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser  
 165 170  
 Thr Ser Thr Thr Phe Gly Arg Thr Val Met  
 175 180  
 Leu Thr Val Gln Phe Thr Leu Gly Trp Pro  
 185 190  
 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg  
 195 200

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Pro Tyr Asp Gly Gly Phe Ala Cys His Phe  
205 210

His Pro Asn Ala Pro Ile Tyr Asn Asp Arg  
215 220

Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala  
225 230

Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu  
235 240

Pro Tyr Ala Ala Val Gln Gly Val Ala Ser  
245 250

Met Val Cys Phe Leu Arg Val Pro Leu Leu  
255 260

Ile Val Asn Gly Phe Leu Val Leu Ile Thr  
265 270

Tyr Leu Gln His Thr His Pro Ser Leu Pro  
275 280

His Tyr Asp Ser Ser Glu Trp Asp Trp Leu  
285 290

Arg Gly Ala Leu Ala Thr Val Asp Arg Asp  
295 300

Tyr Gly Ile Leu Asn Gln Gly Phe His Asn  
305 310

Ile Thr Asp Thr His Glu Ala His His Leu  
315 320

Phe Ser Thr Met Pro His Tyr His Ala Met  
325 330

Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu  
335 340

Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro  
345 350

Val Val Lys Ala Met Trp Arg Glu Ala Lys  
355 360

Glu Cys Ile Tyr Val Glu Pro Asp Arg Gln  
365 370

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Asn Lys Leu Xaa

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Leu Asn Asn Pro Leu Gly Arg Ala Val  
115 120

Sub  
at  
cont

Ser Leu Leu Val Thr Leu Thr Ile Gly Trp  
 125 130  
 Pro Met Tyr Leu Ala Phe Asn Val Ser Gly  
 135 140  
 Arg Pro Tyr Asp Ser Phe Ala Ser His Tyr  
 145 150  
 His Pro Tyr Arg Val Arg Leu Leu Ile Tyr  
 155 160  
 Val Ser Asp Val Ala Leu Phe Ser Val Thr  
 165 170  
 Tyr Ser Leu Tyr Arg Val Ala Thr Leu Lys  
 175 180  
 Gly Leu Val Trp Leu Leu Cys Val Tyr Gly  
 185 190  
 Val Pro Leu Leu Ile Val Asn Gly Phe Leu  
 195 200  
 Val Thr Ile Thr Tyr Leu Arg Val His Tyr  
 205 210  
 Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly  
 215 220  
 Ala Leu Ala Thr Met Asp Arg Asp Tyr Gly  
 225 230  
 Ile Leu Asn Lys Val Phe His His Ile Thr  
 235 240  
 Asp Thr His Val Ala His His Leu Phe Ser  
 245 250  
 Thr Met Pro His Tyr His Leu Arg Val Lys  
 255 260  
 Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp  
 265 270  
 Asp Thr Pro Phe Tyr Lys Ala Leu Trp Arg  
 275 280  
 Glu Ala Arg Glu Cys Leu Tyr Val Glu Pro  
 285 290

Sub  
 at  
 Cont



Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr  
295 300

Trp Tyr Arg Asn Lys Tyr Leu Arg Val  
305

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile  
5 10

Ala Phe Cys Leu Tyr Tyr Val Ala Thr His  
15 20

Tyr Phe His Leu Leu Pro Gly Pro Leu Ser  
25 30

Phe Arg Gly Met Ala Ile Tyr Trp Ala Val  
35 40

Gln Gly Cys Ile Leu Thr Gly Val Trp Val  
45 50

Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp  
55 60

Asp Ile Val Gly Leu Ile Leu His Ser Ala  
65 70

Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
75 80

Ser His Arg Arg His His Ser Asn Thr Gly  
85 90

Ser Leu Glu Arg Asp Glu Val Phe Val Pro  
95 100

Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro  
105 110

Gly Arg Val Leu Thr Leu Ala Val Thr Leu  
115 120

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cont*

Thr Leu Gly Trp Pro Leu Tyr Leu Ala Leu  
 125 130  
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe  
 135 140  
 Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile  
 145 150  
 Tyr Ser Val Ile Ser Asp Ala Gly Val Leu  
 155 160  
 Ala Val Val Tyr Gly Leu Phe Arg Leu Ala  
 165 170  
 Met Ala Lys Gly Leu Ala Trp Val Val Cys  
 175 180  
 Val Tyr Gly Val Pro Leu Leu Val Val Asn  
 185 190  
 Gly Phe Leu Val Leu Ile Thr Phe Leu Gln  
 195 200  
 His Thr His Val Ser Glu Trp Asp Trp Leu  
 205 210  
 Arg Gly Ala Leu Ala Thr Val Asp Arg Asp  
 215 220  
 Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
 225 230  
 Ile Thr Asp Thr His Val Ala His His Leu  
 235 240  
 Phe Ser Thr Met Pro His Tyr His Ala Met  
 245 250  
 Glu Ala Thr Val Glu Tyr Tyr Arg Phe Asp  
 255 260  
 Glu Thr Pro Phe Val Lys Ala Met Trp Arg  
 265 270  
 Glu Ala Arg Glu Cys Ile Tyr Val Glu Pro  
 275 280  
 Asp Gln Ser Thr Glu Ser Lys Gly Val Phe  
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Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala  
295 300

Thr Val

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Ala Gly Gly Arg Met Thr Glu Lys  
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Glu Arg Glu Lys Gln Glu Gln Leu Ala Arg  
15 20

Ala Thr Gly Gly Ala Ala Met Gln Arg Ser  
25 30

Pro Val Glu Lys Pro Pro Phe Thr Leu Gly  
35 40

Gln Ile Lys Lys Ala Ile Pro Pro His Cys  
45 50

Phe Glu Arg Ser Val Leu Lys Ser Phe Ser  
55 60

Tyr Val Val His Asp Leu Val Ile Ala Ala  
65 70

Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile  
75 80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala  
85 90

Ala Trp Pro Leu Tyr Trp Ile Ala Gln Gly  
95 100

Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp  
105 110

Val Val Gly Leu Val Leu His Ser Ser Leu  
115 120

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Met Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 125 130  
 His Arg Arg His His Ser Asn Thr Gly Ser  
 135 140  
 Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150  
 Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro  
 155 160  
 Tyr Val Tyr Asn Asn Pro Val Gly Arg Val  
 165 170  
 Val His Ile Val Val Gln Leu Thr Leu Gly  
 175 180  
 Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser  
 185 190  
 Gly Arg Pro Tyr Pro Arg Phe Ala Cys His  
 195 200  
 Phe Asp Pro Tyr Gly Pro Ile Tyr Asn Asp  
 205 210  
 Arg Glu Arg Ala Gln Ile Phe Val Ser Asp  
 215 220  
 Ala Gly Val Val Ala Val Ala Phe Gly Leu  
 225 230  
 Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp  
 235 240  
 Trp Val Val Arg Val Tyr Ala Val Pro Leu  
 245 250  
 Leu Ile Val Asn Ala Trp Leu Val Leu Ile  
 255 260  
 Thr Tyr Leu Gln His Thr His Pro Ser Leu  
 265 270  
 Pro His Tyr Asp Ser Ser Glu Trp Asp Trp  
 275 280  
 Leu Arg Gly Ala Leu Ala Thr Met Asp Arg  
 285 290

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Asp Tyr Gly Ile Leu Asn Arg Val Phe His  
 295 300  
 Asn Ile Thr Asp Thr His Val Ala His His  
 305 310  
 Leu Phe Ser Thr Met Pro His Tyr His Ala  
 315 320  
 Met Glu Ala Thr Lys Ala Ile Arg Pro Ile  
 325 330  
 Leu Gly Asp Tyr Tyr His Phe Asp Pro Thr  
 335 340  
 Pro Val Ala Lys Ala Thr Trp Arg Glu Ala  
 345 350  
 Gly Glu Cys Ile Tyr Val Glu Pro Glu Asp  
 355 360  
 Arg Lys Gly Val Phe Trp Tyr Asn Lys Lys  
 365 370  
 Phe Xaa

## (2) INFORMATION FOR SEQ ID NO:11

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Trp Val Met Ala His Asp Cys Gly His His  
 5 10  
 Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp  
 15 20  
 Val Val Gly Leu Ile Leu His Ser Cys Leu  
 25 30  
 Leu Val Pro Tyr Phe Ser Trp Lys His Ser  
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 His Arg Arg His His Ser Asn Thr Gly Ser  
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Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 55 60  
 Lys Lys Ser Ser Ile Arg Trp Tyr Ser Lys  
 65 70  
 Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met  
 75 80  
 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp  
 85 90  
 Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly  
 95 100  
 Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr  
 105 110  
 Asp Pro Tyr Gly Pro Ile Tyr Asn Asp Arg  
 115 120  
 Glu Arg Ile Glu Ile Phe Ile Ser Asp Ala  
 125 130  
 Gly Val Leu Ala Val Thr Phe Gly Leu Tyr  
 135 140  
 Gln Leu Ala Ile Ala Lys Gly Leu Ala Trp  
 145 150  
 Val Val Cys Val Tyr Gly Val Pro Leu Leu  
 155 160  
 Val Val Asn Ser Phe Leu Val Leu Ile Thr  
 165 170  
 Phe Leu Gln His Thr His Pro Ala Leu Pro  
 175 180  
 His Tyr Asp Ser Ser Glu Trp Asp Trp Leu  
 185 190  
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 195 200  
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 205 210  
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(2) INFORMATION FOR SEQ ID NO:12

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTCTTTTGT GCGCTCATTC

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(2) INFORMATION FOR SEQ ID NO:13

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGTACCAGA AAAGGCCTTG

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(2) INFORMATION FOR SEQ ID NO:14

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAYWSNCAYM GNMGNCA YCA

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(2) INFORMATION FOR SEQ ID NO:15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

RTGRTGNGCN ACRTGNGTRT C

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